

SEQUENCE LISTING

(1) GENERAL INFORMATION:

(i) APPLICANT: Tobin, James

(ii) TITLE OF INVENTION: HUMAN INTERLUKIN-11 RECEPTOR

(iii) NUMBER OF SEQUENCES: 4

(iv) CORRESPONDENCE ADDRESS:

(A) ADDRESSEE: Genetics Institute, Inc.

(B) STREET: 87 CambridgePark Drive

(C) CITY: Cambridge

(D) STATE: MA

(E) COUNTRY: USA

(F) ZIP: 02140

(v) COMPUTER READABLE FORM:

(A) MEDIUM TYPE: Floppy disk

(B) COMPUTER: IBM PC compatible

(C) OPERATING SYSTEM: PC-DOS/MS-DOS

(D) SOFTWARE: PatentIn Release #1.0, Version #1.25

(vi) CURRENT APPLICATION DATA:

(A) APPLICATION NUMBER:

(B) FILING DATE:

(C) CLASSIFICATION:

(viii) ATTORNEY/AGENT INFORMATION:

(A) NAME: Brown, Scott A.

(B) REGISTRATION NUMBER: 32,724

(C) REFERENCE/DOCKET NUMBER: GI5252

(ix) TELECOMMUNICATION INFORMATION:

(A) TELEPHONE: (617) 498-8224

(B) TELEFAX: (617) 876-5851

(2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2456 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 734..1999

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

TCGCCCCACCC	CCAGCCTCTG	GCAGCAGCCA	GGGCATCTGG	ATCTGCTTAA	CTACACAGCC	60
CCAGCCTGCA	CCCTAGCCCC	ATCCAGCTTC	ACAAACTGGA	GACCAACGAA	GTGTCAAGAG	120
CCAGGCCCCAG	CTGAGTGGCC	CAAGTAGCCA	GACCAAGGAG	CCAGGTTTCAG	GCGAGAAGCC	180
TGGCAGCCAG	GGCAGGGGTG	GGCCTCAGGG	TGGGAGTGCA	GGATGGGCTC	AGATCCATGA	240
TGACACCCCTT	CCCCCAGGGT	GATAAGGTCT	GCCTAGGTTA	ATCAGAGGCA	GTGATAAGCC	300
CTGGACCAGG	TGGGGGTAAA	TACCAGAATT	CCCAACAGCT	GGACTGGAGG	GGTTAATGGG	360
ACTGGCTGAG	CTGGTGCCAG	TGCTTGGTGC	CAGGGGTGGG	CGCCAAGGGC	AGTGGAGGGG	420
GAGTTGCTGG	CACAGTCTGT	TGCCTCCGGC	TTTTGTTCTG	GGCCCTAAGC	CCAGGACTGA	480
GATGGAGGGT	GTGAGGGGGT	GTGTGTGTCC	GTGTGTGTGT	GTGTGTGTGT	GTGCGCGCGC	540
ACGCACATGC	AAAGCACTGG	GTATACAGTG	GGAAAGGGGA	CCTCAGGTCA	GTTCCCCGCAG	600

PROTEIN SEQUENCE

TGATTTCTAA CAGCCTTACC CCACTTGGTG CATCAATTTT TCTCCTAGGA AGCCTCAGTT 660
 TTGGAGAGGA AGAGCCAGGC TTTAGCCTCC CATCTCAGGG GTCGGGGATT TTTGACTCTA 720
 CCTCTCCCA CAG ATG AGC AGC AGC TGC TCA GGG CTG AGC AGG GTC CTG 769
 Met Ser Ser Ser Cys Ser Gly Leu Ser Arg Val Leu 10
 1
 GTG GCC GTG GCT ACA GCC CTG GTG TCT GCC TCC TCC CCC TGC CCC CAG 817
 Val Ala Val Ala Thr Ala Leu Val Ser Ala Ser Ser Pro Cys Pro Gln 25
 15 20
 GCC TGG GGC CCC CCA GGG GTC CAG TAT GGG CAG CCA GGC AGG TCC GTG 865
 Ala Trp Gly Pro Pro Gly Val Gln Tyr Gly Gln Pro Gly Arg Ser Val 40
 30 35
 AAG CTG TGT TGT CCT GGA GTG ACT GCC GGG GAC CCA GTG TCC TGG TTT 913
 Lys Leu Cys Cys Pro Gly Val Thr Ala Gly Asp Pro Val Ser Trp Phe 60
 45 50
 CGG GAT GGG GAG CCA AAG CTG CTC CAG GGA CCT GAC TCT GGG CTA GGG 961
 Arg Asp Gly Glu Pro Lys Leu Leu Gln Gly Pro Asp Ser Gly Leu Gly 75
 65 70
 CAT GAA CTG GTC CTG GCC CAG GCA GAC AGC ACT GAT GAG GGC ACC TAC 1009
 His Glu Leu Val Leu Ala Gln Ala Asp Ser Thr Asp Glu Gly Thr Tyr 90
 80
 ATC TGC CAG ACC CTG GAT GGT GCA CTT GGG GGC ACA GTG ACC CTG CAG 1057
 Ile Cys Gln Thr Leu Asp Gly Ala Leu Gly Gly Thr Val Thr Leu Gln 105
 95 100
 CTG GGC TAC CCT CCA GCC CGC CCT GTT GTC TCC TGC CAA GCA GCC GAC 1105
 Leu Gly Tyr Pro Pro Ala Arg Pro Val Val Ser Cys Gln Ala Ala Asp 120
 110 115
 TAT GAG AAC TTC TCT TGC ACT TGG AGT CCC AGC CAG ATC ACC GGT TTA 1153
 Tyr Glu Asn Phe Ser Cys Thr Trp Ser Pro Ser Gln Ile Ser Gly Leu 140
 125 130 135

Table 3: Sequence

CCC ACC CGC TAC CTC ACC TCC TAC AGG AAG ACA GTC CTA GGA GCT Pro Thr Arg Tyr Leu Thr Ser Tyr Arg Lys Lys Thr Val Leu Gly Ala 145 150 155	1201
GAT AGC CAG AGG AGT CCA TCC ACA GGG CCC TGG CCA TGC CCA CAG Asp Ser Gln Arg Arg Ser Pro Ser Thr Gly Pro Trp Pro Cys Pro Gln 160 165 170	1249
GAT CCC CTA GGG GCT GCC CGC TGT GTT GTC CAC GGG GCT GAG TTC TGG Asp Pro Leu Gly Ala Ala Arg Cys Val Val His Gly Ala Glu Phe Trp 175 180 185	1297
AGC CAG TAC CGG ATT AAT GTG ACT GAG GTG AAC CCA CTG GGT GCC AGC Ser Gln Tyr Arg Ile Asn Val Thr Glu Val Asn Pro Leu Gly Ala Ser 190 195 200	1345
ACA CGC CTG CTG GAT GTG AGC TTG CAG AGC ATC TTG CGC CCT GAC CCA Thr Arg Leu Leu Asp Val Ser Leu Gln Ser Ile Leu Arg Pro Asp Pro 205 210 220	1393
CCC CAG GGC CTG CGG GTA GAG TCA GTA CCA GGT TAC CCC CGA CGC CTG Pro Gln Gly Leu Arg Val Glu Ser Val Pro Gly Tyr Pro Arg Arg Leu 225 230 235	1441
CGA GCC AGC TGG ACA TAC CCT GCC TCC TGG CCG TGC CAG CCC CAC TTC Arg Ala Ser Trp Thr Tyr Pro Ala Ser Trp Pro Cys Gln Pro His Phe 240 245 250	1489
CTG CTC AAG TTC CGT TTG CAG TAC CGT CCG GCG CAG CAT CCA GCC TGG Leu Leu Lys Phe Arg Leu Gln Tyr Arg Pro Ala Gln His Pro Ala Trp 255 260 265	1537
TCC ACG GTG GAG CCA GCT GGA CTG GAG GTG ATC ACA GAT GCT GTG Ser Thr Val Glu Pro Ala Gly Leu Glu Val Ile Thr Asp Ala Val 270 275 280	1585
GCT GGG CTG CCC CAT GCT GTA CGA GTC AGT GCC CGG GAC TTT CTA GAT Ala Gly Leu Pro His Ala Val Arg Val Ser Ala Arg Asp Phe Leu Asp 285 290 295 300	1633

Sequence

CATGTGCTG TGAGGCAGG AACATGTATT CTCTGCATGC ATGTATGTAG GTGCCTGGG 2319
 AGTGTGTGTG GGTCTTGGC TCTTGGCCTT TCCCTTGCA GGGTTGTGC AGGTGTGAAT 2379
 AAGAGAATA AGGAAGTTCT TGGAGATTAT ACTCAGAAAA AAAAAAAAAA AGTCGACGCG 2439
 GCCGCGAATT CCTGCAG 2456

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 422 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

Met Ser Ser Ser Cys Ser Gly Leu Ser Arg Val Leu Val Ala Val Ala 15
 1
 Thr Ala Leu Val Ser Ala Ser Ser Pro Cys Pro Gln Ala Trp Gly Pro 30
 20
 Pro Gly Val Gln Tyr Gly Gln Pro Gly Arg Ser Val Lys Leu Cys Cys 45
 35
 Pro Gly Val Thr Ala Gly Asp Pro Val Ser Trp Phe Arg Asp Gly Glu 60
 50
 Pro Lys Leu Leu Gln Gly Pro Asp Ser Gly Leu Gly His Glu Leu Val 80
 65
 Leu Ala Gln Ala Asp Ser Thr Asp Glu Gly Thr Tyr Ile Cys Gln Thr 95
 85
 Leu Asp Gly Ala Leu Gly Thr Val Thr Leu Gln Leu Gly Tyr Pro 110
 100

Protein Sequence

Pro Ala Arg Pro Val Val Ser Cys Gln Ala Ala Asp Tyr Glu Asn Phe
 115 120
 Ser Cys Thr Trp Ser Pro Ser Gln Ile Ser Gly Leu Pro Thr Arg Tyr
 130 135 140
 Leu Thr Ser Tyr Arg Lys Lys Thr Val Leu Gly Ala Asp Ser Gln Arg
 145 150 155 160
 Arg Ser Pro Ser Thr Gly Pro Trp Pro Cys Pro Gln Asp Pro Leu Gly
 165 170 175
 Ala Ala Arg Cys Val Val His Gly Ala Glu Phe Trp Ser Gln Tyr Arg
 180 185 190
 Ile Asn Val Thr Glu Val Asn Pro Leu Gly Ala Ser Thr Arg Leu Leu
 195 200 205
 Asp Val Ser Leu Gln Ser Ile Leu Arg Pro Asp Pro Pro Gln Gly Leu
 210 215 220
 Arg Val Glu Ser Val Pro Gly Tyr Pro Arg Arg Leu Arg Ala Ser Trp
 225 230 235 240
 Thr Tyr Pro Ala Ser Trp Pro Cys Gln Pro His Phe Leu Leu Lys Phe
 245 250 255
 Arg Leu Gln Tyr Arg Pro Ala Gln His Pro Ala Trp Ser Thr Val Glu
 260 265 270
 Pro Ala Gly Leu Glu Glu Val Ile Thr Asp Ala Val Ala Gly Leu Pro
 275 280 285
 His Ala Val Arg Val Ser Ala Arg Asp Phe Leu Asp Ala Gly Thr Trp
 290 295 300
 Ser Thr Trp Ser Pro Glu Ala Trp Gly Thr Pro Ser Thr Gly Thr Ile
 305 310 315 320
 Pro Lys Glu Ile Pro Ala Trp Gly Gln Leu His Thr Gln Pro Glu Val

LOCUS: B24250

325		330	335
Glu Pro Gln Val Asp Ser Pro Ala Pro Pro Arg Pro Ser Leu Gln Pro			
340	345		350
His Pro Arg Leu Leu Asp His Arg Asp Ser Val Glu Gln Val Ala Val			
355	360		365
Leu Ala Ser Leu Gly Ile Leu Ser Phe Leu Gly Leu Val Ala Gly Ala			
370	375	380	
Leu Ala Leu Gly Leu Trp Leu Arg Leu Arg Arg Gly Gly Lys Asp Gly			
385	390	395	400
Ser Pro Lys Pro Gly Phe Leu Ala Ser Val Ile Pro Val Asp Arg Arg			
405	410	415	
Pro Gly Ala Pro Asn Leu			
420			

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1714 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 34..1359

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

THE "SECRET"

TTCTTAGCCT GATAGGAGGA AGTCTTGGAG GCC ATG GCA CTC AGT CAC TGT GAT 54
 Met Ala Leu Ser His Cys Asp 1 5

 TAT CAA GAT GAG CAG CTG CTC AGG GCT GAC CAG GGT CCT GGT GGC 102
 Tyr Gln Asp Glu Gln Gln Leu Leu Arg Ala Asp Gln Gly Pro Gly Gly 10 20

 CGT GCT ACA GCC CTG GTG TCT TCC TCC CCC TGC CCC CAA GCT TGG 150
 Arg Ala Thr Ala Leu Val Ser Ser Ser Pro Cys Pro Gln Ala Trp 25 30 35

 GGT CCT CCA GGG GTC CAG TAT GGA CAA CCT GGC AGG CCC GTG ATG CTG 198
 Gly Pro Pro Gly Val Gln Tyr Gly Gln Pro Gly Arg Pro Val Met Leu 40 45 50 55

 TGC TGC CCC GGA GTG AGT GCT GGG ACT CCA GTG TCC TGG TTT CGG GAT 246
 Cys Cys Pro Gly Val Ser Ala Gly Thr Pro Val Ser Trp Phe Arg Asp 60 65 70

 GGA GAT TCA AGG CTG CTC CAG GGA CCT GAC TCT GGG TTA GGA CAC AGA 294
 Gly Asp Ser Arg Leu Leu Gln Gly Pro Asp Ser Gly Leu Gly His Arg 75 80 85

 CTG GTC TTG GCC CAG GTG GAC AGC CCT GAT GAA GGC ACT TAT GTC TGC 342
 Leu Val Leu Ala Gln Val Asp Ser Pro Asp Glu Gly Thr Tyr Val Cys 90 95 100

 CAG ACC CTG GAT GGT GTA TCA GGG GGC ATG GTG ACC CTG AAG CTG GGC 390
 Gln Thr Leu Asp Gly Val Ser Gly Gly Met Val Thr Leu Lys Leu Gly 105 110 115

 TTT CCC CCA GCA CGT CCT GAA GTC TCC TGC CAA GCG GTA GAC TAT GAA 438
 Phe Pro Pro Ala Arg Pro Glu Val Ser Cys Gln Ala Val Asp Tyr Glu 120 125 130 135

 AAC TTC TCC TGT ACT TGG AGT CCA GGC CAG GTC AGC GGT TTG CCC ACC 486
 Asn Phe Ser Cys Thr Trp Ser Pro Gly Gln Val Ser Gly Leu Pro Thr 140 145 150

THE SEED

CGC TAC CTT ACT TCC TAC AGG AAG AAG ACG CTG CCA GGA GCT GAG AGT 534
 Arg Tyr Leu 155
 Thr Ser Tyr Arg Lys Lys Thr Leu Pro Gly Ala Glu Ser 165

CAG AGG GAA AGT CCA TCC ACC GGG CCT TGG CCG TGT CCA CAG GAC CCT 582
 Gln Arg Glu Ser Pro Ser Thr Gly Pro Trp Pro Cys Pro Gln Asp Pro 175
 170

CTG GAG GCC TCC CGA TGT GTG GTC CAT GGG GCA GAG TTC TGG AGT GAG 630
 Leu Glu Ala Ser Arg Cys Val Val His Gly Ala Glu Phe Trp Ser Glu 185
 190 195

TAC CGG ATC AAT GTG ACC GAG GTG AAC CCA CTG GGT GCC AGC ACG TGC 678
 Tyr Arg Ile Asn Val Thr Glu Val Asn Pro Leu Gly Ala Ser Thr Cys 200
 205 210 215

CTA CTG GAT GTG AGA TTA CAG AGC ATC TTG CGT CCT GAT CCA CCC CAA 726
 Leu Leu Asp Val Arg Leu Gln Ser Ile Leu Arg Pro Asp Pro Pro Gln 220
 225 230

GGA CTG CGG GTG GAA TCC GTA CCT GGT TAC CCG AGA CGC CTG CAT GCC 774
 Gly Leu Arg Val Glu Ser Val Pro Gly Tyr Pro Arg Arg Leu His Ala 235
 240 245

AGC TGG ACA TAC CCT GCC TCC TGG CGT CGC CAA CCC CAC TTT CTG CTC 822
 Ser Trp Thr Tyr Pro Ala Ser Trp Arg Arg Gln Pro His Phe Leu Leu 250
 255 260

AAG TTC CGG TTG CAA TAC CGA CCA GCA CAG CAT CCA GCC TGG TCC ACG 870
 Lys Phe Arg Leu Gln Tyr Arg Pro Ala Gln His Pro Ala Trp Ser Thr 265
 270 275

GTG GAG CCC ATT GGC TTG GAG GAA GTG ATA ACA GAT GCT GTG GCT GGG 918
 Val Glu Pro Ile Gly Leu Glu Glu Val Ile Thr Asp Ala Val Ala Gly 280
 285 290 295

CTG CCA CAC GCG GTA CGA GTC AGT GCC AGG GAC TTT CTG GAT GCT GGC 966
 Leu Pro His Ala Val Arg Val Ser Ala Arg Asp Phe Leu Asp Ala Gly 300
 305 310

TABLE 1

ACC TGG AGC GCC TGG AGC CCA GAG GCC TGG GGT ACT CCT AGC ACT GGT Thr Trp Ser Ala Trp Ser Pro Glu Ala Trp Gly Thr Pro Ser Thr Gly 315 320 325	1014
CCC CTG CAG GAT GAG ATA CCT GAT TGG AGC CAG GGA CAT GGA CAG CAG Pro Leu Gln Asp Glu Ile Pro Asp Trp Ser Gln Gly His Gly Gln Gln 330 335 340	1062
CTA GAG GCA GTA GTA GCT CAG GAG GAC AGC CCG GCT CCT GCA AGG CCT Leu Glu Ala Val Val Ala Gln Glu Asp Ser Pro Ala Pro Ala Arg Pro 345 350 355	1110
TCC TTG CAG CCG GAC CCA AGG CCA CTT GAT CAC AGG GAC CCC TTG GAG Ser Leu Gln Pro Asp Pro Arg Pro Leu Asp His Arg Asp Pro Leu Glu 360 365 370 375	1158
CAA GTA GCT GTG TTA GCG TCT CTG GGA ATC TTC TCT TGC CTT GGC CTG Gln Val Ala Val Leu Ala Ser Leu Gly Ile Phe Ser Cys Leu Gly Leu 380 385 390	1206
GCT GTT GGA GCT CTG GCA CTG GGG CTC TGG CTG AGG CTG AGA CCG AGT Ala Val Gly Ala Leu Ala Leu Gly Leu Trp Leu Arg Leu Arg Arg Ser 395 400 405	1254
GGG AAG GAT GGA CCG CAA AAA CCT GGG CTC TTG GCA CCC ATG ATC CCG Gly Lys Asp Gly Pro Gln Lys Pro Gly Leu Ala Pro Met Ile Pro 410 415 420	1302
GTG GAA AAG CTT CCA GGA ATT CCA AAC CTG CAG AGG ACC CCA GAG AAC Val Glu Lys Leu Pro Gly Ile Pro Asn Leu Gln Arg Thr Pro Glu Asn 425 430 435	1350
TTC AGC TGATTTTCATC TGTAACCCGG TCAGACTTGG GGTGGTTAAA AGGACAGGCA Phe Ser 440	1406
GAAAGAGCGG GGGCAGTGGA TCCCTGTGGA TGGAGGTCTC AGCTGAAAGT CTGAGCTCTT	1466
TTCTTTTGACA CCTATACTCC AAACCTTGCTG CCGGCTGAAG GCTGTCTGGA CTTCGGATGT	1526

Protein Sequence

Met Val Thr Leu Lys Leu Gly Phe Pro Pro Ala Arg Pro Glu Val Ser
 115 120 125

Cys Gln Ala Val Asp Tyr Glu Asn Phe Ser Cys Thr Trp Ser Pro Gly
 130 135 140

Gln Val Ser Gly Leu Pro Thr Arg Tyr Leu Thr Ser Tyr Arg Lys
 145 150 155 160

Thr Leu Pro Gly Ala Glu Ser Gln Arg Glu Ser Pro Ser Thr Gly Pro
 165 170 175

Trp Pro Cys Pro Gln Asp Pro Leu Glu Ala Ser Arg Cys Val Val His
 180 185 190

Gly Ala Glu Phe Trp Ser Glu Tyr Arg Ile Asn Val Thr Glu Val Asn
 195 200 205

Pro Leu Gly Ala Ser Thr Cys Leu Leu Asp Val Arg Leu Gln Ser Ile
 210 215 220

Leu Arg Pro Asp Pro Pro Gln Gly Leu Arg Val Glu Ser Val Pro Gly
 225 230 235 240

Tyr Pro Arg Arg Leu His Ala Ser Trp Thr Tyr Pro Ala Ser Trp Arg
 245 250 255

Arg Gln Pro His Phe Leu Leu Lys Phe Arg Leu Gln Tyr Arg Pro Ala
 260 265 270

Gln His Pro Ala Trp Ser Thr Val Glu Pro Ile Gly Leu Glu Val
 275 280 285

Ile Thr Asp Ala Val Ala Gly Leu Pro His Ala Val Arg Val Ser Ala
 290 295 300

Arg Asp Phe Leu Asp Ala Gly Thr Trp Ser Ala Trp Ser Pro Glu Ala
 305 310 315 320

Trp Gly Thr Pro Ser Thr Gly Pro Leu Gln Asp Glu Ile Pro Asp Trp

THE 1980 EDITION

325	330	335
Ser Gln Gly His Gly Gln Gln Leu Glu Ala Val Val Ala Gln Glu Asp		
340	345	350
Ser Pro Ala Pro Ala Arg Pro Ser Leu Gln Pro Asp Pro Arg Pro Leu		
355	360	365
Asp His Arg Asp Pro Leu Glu Gln Val Ala Val Leu Ala Ser Leu Gly		
370	375	380
Ile Phe Ser Cys Leu Gly Leu Ala Val Gly Ala Leu Ala Leu Gly Leu		
385	390	395
Trp Leu Arg Leu Arg Arg Ser Gly Lys Asp Gly Pro Gln Lys Pro Gly		
405	410	415
Leu Leu Ala Pro Met Ile Pro Val Glu Lys Leu Pro Gly Ile Pro Asn		
420	425	430
Leu Gln Arg Thr Pro Glu Asn Phe Ser		
435	440	

$\frac{1}{2}$ $\frac{1}{3}$ $\frac{1}{4}$ $\frac{1}{5}$ $\frac{1}{6}$ $\frac{1}{7}$ $\frac{1}{8}$ $\frac{1}{9}$ $\frac{1}{10}$ $\frac{1}{11}$ $\frac{1}{12}$ $\frac{1}{13}$ $\frac{1}{14}$ $\frac{1}{15}$ $\frac{1}{16}$ $\frac{1}{17}$ $\frac{1}{18}$ $\frac{1}{19}$ $\frac{1}{20}$ $\frac{1}{21}$ $\frac{1}{22}$ $\frac{1}{23}$ $\frac{1}{24}$ $\frac{1}{25}$ $\frac{1}{26}$ $\frac{1}{27}$ $\frac{1}{28}$ $\frac{1}{29}$ $\frac{1}{30}$ $\frac{1}{31}$ $\frac{1}{32}$ $\frac{1}{33}$ $\frac{1}{34}$ $\frac{1}{35}$ $\frac{1}{36}$ $\frac{1}{37}$ $\frac{1}{38}$ $\frac{1}{39}$ $\frac{1}{40}$ $\frac{1}{41}$ $\frac{1}{42}$ $\frac{1}{43}$ $\frac{1}{44}$ $\frac{1}{45}$ $\frac{1}{46}$ $\frac{1}{47}$ $\frac{1}{48}$ $\frac{1}{49}$ $\frac{1}{50}$ $\frac{1}{51}$ $\frac{1}{52}$ $\frac{1}{53}$ $\frac{1}{54}$ $\frac{1}{55}$ $\frac{1}{56}$ $\frac{1}{57}$ $\frac{1}{58}$ $\frac{1}{59}$ $\frac{1}{60}$ $\frac{1}{61}$ $\frac{1}{62}$ $\frac{1}{63}$ $\frac{1}{64}$ $\frac{1}{65}$ $\frac{1}{66}$ $\frac{1}{67}$ $\frac{1}{68}$ $\frac{1}{69}$ $\frac{1}{70}$ $\frac{1}{71}$ $\frac{1}{72}$ $\frac{1}{73}$ $\frac{1}{74}$ $\frac{1}{75}$ $\frac{1}{76}$ $\frac{1}{77}$ $\frac{1}{78}$ $\frac{1}{79}$ $\frac{1}{80}$ $\frac{1}{81}$ $\frac{1}{82}$ $\frac{1}{83}$ $\frac{1}{84}$ $\frac{1}{85}$ $\frac{1}{86}$ $\frac{1}{87}$ $\frac{1}{88}$ $\frac{1}{89}$ $\frac{1}{90}$ $\frac{1}{91}$ $\frac{1}{92}$ $\frac{1}{93}$ $\frac{1}{94}$ $\frac{1}{95}$ $\frac{1}{96}$ $\frac{1}{97}$ $\frac{1}{98}$ $\frac{1}{99}$ $\frac{1}{100}$

GCT GGC ACC TGG AGC ACC TGG AGC CCG GAG GCC TGG GGA ACT CCG AGC Ala Gly Thr Trp Ser Thr Trp Ser Pro Glu Ala Trp Gly Thr Pro Ser 305 310 315	1681
ACT GGG ACC ATA CCA AAG GAG ATA CCA GCA TGG GGC CAG CTA CAC ACG Thr Gly Thr Ile Pro Lys Glu Ile Pro Ala Trp Gly Gln Leu His Thr 320 325 330	1729
CAG CCA GAG GTG GAG CCT CAG GTG GAC AGC CCT GCT CCT CCA AGG CCC Gln Pro Glu Val Glu Pro Gln Val Asp Ser Pro Ala Pro Pro Arg Pro 335 340 345	1777
TCC CTC CAA CCA CAC CCT CGG CTA CTT GAT CAC AGG GAC TCT GTG GAG Ser Leu Gln Pro His Pro Arg Leu Leu Asp His Arg Asp Ser Val Glu 350 355 360	1825
CAG GTA GCT GTG CTG GCG TCT TTG GGA ATC CTT TCT TTC CTG GGA CTG Gln Val Ala Val Leu Ala Ser Leu Gly Ile Leu Ser Phe Leu Gly Leu 365 370 375	1873
GTG GCT GGG GCC CTG GCA CTG GGG CTC TGG CTG AGG CTG AGA CGG GGT Val Ala Gly Ala Leu Ala Leu Gly Leu Trp Leu Arg Leu Arg Arg Gly 385 390 395	1921
GGG AAG GAT GGA TCC CCA AAG CCT GGG TTC TTG GCC TCA GTG ATT CCA Gly Lys Asp Gly Ser Pro Lys Pro Gly Phe Leu Ala Ser Val Ile Pro 400 405 410	1969
GTG GAC AGG CGT CCA GGA GCT CCA AAC CTG TAGAGGACCC AGGAGGGCTT Val Asp Arg Arg Pro Gly Ala Pro Asn Leu 415 420	2019
CGGCAGATT CACCTATAAT TCTGTCTTGC TGGTGTGGAT GGATGGACAG ATAGAAACCA	2079
GGCAGGACAG TAGATCCCTA TGGTTGGATC TCAGCTGGAA GTTCTGTTTG GAGCCATT	2139
CTGTGAGACC CTGTAATTCA AATTGTCAGC TGAAAGGTGC TTGTACCTCT GATTTCACCC	2199
CAGAGTTGGA GTTCTGCTCA AGGAACGTGT GTAATGTGTA CATCTGTGTC CATGTGTGAC	2259